

AUSTRALIA

Patents Act 1990

IN THE MATTER OF Australian Patent
Application Serial No 696764 by Human
Genome Sciences, Inc.

-and-

IN THE MATTER OF Opposition thereto by
Ludwig Institute for Cancer Research

THIS IS Exhibit 2 referred to in the Statutory Declaration of Kari Alitalo made
before me this 15th Day of February, 2000

OLLI-PEKKA SIRO
~~Notary Public~~
Notary Public



EXHIBIT 2

Nucleotide and Amino Acid Sequence of VEGF-C and primers to make VEGF2(HGS)

The 5' and 3' primers used in the PCR reaction are indicated in capital letters. The BamHI site in the 5' primer and the XbaI site in the 3' primer are underlined. The 3' primer also encodes an HA-tag 3' to the last codon of VEGF-C (which encodes a serine), followed by a stop codon indicated in boldface.

ccacccctgc ccccgccagc ggaccgggtcc cccacccccg gtccttccac c atg cac 357
Met His
1

ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg 405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
5 10 15

ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc 453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe Glu Ser
20 25 30

gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
35 40 45 50

tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
55 60 65

5'-CGC GGA TCC ATG ACT GTA CTC TAC CCA-3' 5' Primer

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
70 75 80

tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
85 90 95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
100 105 110

aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa 741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
115 120 125 130

tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
135 140 145

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt 837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
150 155 160

ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg 885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
165 170 175

agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa 933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
180 185 190

ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga	981
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
195 200 205 210	
tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga	1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
215 220 225	
cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc	1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
230 235 240	
tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct	1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
245 250 255	
cag gaa gat ttt atg ttt tcc tgc gat gct gga gat gac tca aca gat	1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
260 265 270	
gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc	1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
275 280 285 290	
tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc	1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
295 300 305	
cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa	1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
310 315 320	
ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca	1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
325 330 335	
tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat	1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
340 345 350	
cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg	1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
355 360 365 370	
tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg	1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
375 380 385	
cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt	1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	
390 395 400	
3'Primer 3' TCT GGT GTT TAC	
gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg	1605
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met	
405 410 415	
TCG GAG CTC ATG GGT ATG CTG CAG GGT CTG ATG CGA ACT <u>AGA TCT</u> CGC-5'	
agc taagattgta ctgttttcca gttcatcgat tttctattat ggaaaactgt	1658
Ser	